TOWARDS THE CONSTRUCTION OF A HIGH DENSITY GENETIC LINKAGE MAP OF WHEAT CHROMOSOME 5A


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A high density genetic map is needed for anchoring BAC contigs during the construction of a physical map and for DNA sequence assembly. The International Wheat Genome Sequencing Consortium is dedicated to the development of physical maps of individual chromosomes as the first step towards the whole genome sequencing of hexaploid wheat. To undertake this challenge for wheat chromosome 5A, we rely on several mapping populations and different parallel approaches for marker development. Three mapping populations are being used: 1) a Chinese Spring x Renan (CSxR) F2 population; 2) an F2 population derived from CS x CS-\textit{Triticum dicoccoides} disomic substitution line for chromosome 5A and, 3) a RIL (Recombinant Inbred Lines) population derived from Langdon (LDN) x LDN-T. \textit{dicoccoides} disomic substitution line for chromosome 5A. For marker development, a Diversity Array Technology (DArT) platform specific for the short and long arms of wheat chromosome 5A has been established using DNA from flow sorted chromosomes, and includes more than 6000 wheat probes. So far, this array is under hybridization with one population (CS x R) while the other two populations are in the pipeline. Besides the DArTs, a set of SSR, RFLP-derived and EST-derived PCR-based markers, specific for 5AS and/or 5AL chromosome arms have been selected from databases and literature. After the assignment to chromosome 5A, performed using CS deletion and aneuploid lines, the markers are being tested for
polymorphism between the parents of the three mapping populations. Polymorphic DNA fragments, specific for 5A, will be mapped in the available population(s). The resulting genetic linkage map of the wheat chromosome 5A will be presented.